COPY

SEQUENCE LISTING

<110> Hodge, Martin R.

<120> 14189, A Novel Human Kinase and Uses Thereof

<130> 5800-153

<140> 09/641,690
<141> 2000-08-18

<160> 13

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<222> (48)...(1682)

<221> misc_feature
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Val Val Asp Pro Arg Ile Val Arg Arg Tyr Leu Leu Arg Arg Gln Leu
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ggg cag ggg gcc tat ggc att gtg tgg aag gca gtg gac cgg agg act      152
Gly Gln Gly Ala Tyr Gly Ile Val Trp Lys Ala Val Asp Arg Arg Thr
 20                  25                  30                  35

ggt gag gtc gtg gcc atc aag aaa atc ttt gat gct ttt agg gat aag      200
Gly Glu Val Val Ala Ile Lys Lys Ile Phe Asp Ala Phe Arg Asp Lys
                 40                  45                  50

aca gat gcc cag aga aca ttc cgg gaa atc acg ctc ctc cag gag ttt      248
Thr Asp Ala Gln Arg Thr Phe Arg Glu Ile Thr Leu Leu Gln Glu Phe
             55                  60                  65

ggg gac cat ccc aac atc atc agc ctc ctt gac gtg atc cgg gca gag      296
Gly Asp His Pro Asn Ile Ile Ser Leu Leu Asp Val Ile Arg Ala Glu
         70                  75                  80

aac gac agg gac att tac ctg gtg ttt gag ttt atg gac act gac ctg      344
Asn Asp Arg Asp Ile Tyr Leu Val Phe Glu Phe Met Asp Thr Asp Leu
     85                  90                  95
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aac gca gtc atc cgg aag ggc ggc ctg ctg cag gac gtc cac gtg cgc      392
Asn Ala Val Ile Arg Lys Gly Gly Leu Leu Gln Asp Val His Val Arg
100                 105                 110                 115

tcc atc ttc tac cag ctc ctg cgg gcc acc cgg ttc ctc cac tcg ggg      440
Ser Ile Phe Tyr Gln Leu Leu Arg Ala Thr Arg Phe Leu His Ser Gly
                120                 125                 130

cac gtt gtg cac cgg gac cag aag ccg tcc aat gtg ctc ctg gat gcc      488
His Val Val His Arg Asp Gln Lys Pro Ser Asn Val Leu Leu Asp Ala
            135                 140                 145

aac tgc aca gtg aag ctg tgt gac ttt ggc ctg gcc cgc tcc ctg ggc      536
Asn Cys Thr Val Lys Leu Cys Asp Phe Gly Leu Ala Arg Ser Leu Gly
        150                 155                 160

gac ctc cct gag ggg cct gag gac cag gcc gtg aca gag tac gtg gcc      584
Asp Leu Pro Glu Gly Pro Glu Asp Gln Ala Val Thr Glu Tyr Val Ala
    165                 170                 175

aca cgc tgg tac cga gca ccg gag gtg ctg ctc tct tcg cac cga tac      632
Thr Arg Trp Tyr Arg Ala Pro Glu Val Leu Leu Ser Ser His Arg Tyr
180                 185                 190                 195

acc ctt ggg gtg gac atg tgg agt ctg ggc tgt atc ctg ggg gag atg      680
Thr Leu Gly Val Asp Met Trp Ser Leu Gly Cys Ile Leu Gly Glu Met
                200                 205                 210

ctg cgg ggg aga ccc ctg ttc ccc ggc acg tcc acc ctn cac cag ctg      728
Leu Arg Gly Arg Pro Leu Phe Pro Gly Thr Ser Thr Xaa His Gln Leu
            215                 220                 225

gag ctg atc ctg gag acc atc cca ccg cca tct gag gag gac ctc ctg      776
Glu Leu Ile Leu Glu Thr Ile Pro Pro Pro Ser Glu Glu Asp Leu Leu
        230                 235                 240

gct ctc ggc tca ggc tgc cgt gcc tct gtg ctg cac cag ctg ggg tcc      824
Ala Leu Gly Ser Gly Cys Arg Ala Ser Val Leu His Gln Leu Gly Ser
    245                 250                 255

cgg cca cga cag acg ctg gat gcc ctc cta ccg cca gac acc tcc cca      872
Arg Pro Arg Gln Thr Leu Asp Ala Leu Leu Pro Pro Asp Thr Ser Pro
260                 265                 270                 275

gag gcc ttg gac ctc ctt agg cga ctc ctg gtg ttc gcc ccg gac aag      920
Glu Ala Leu Asp Leu Leu Arg Arg Leu Leu Val Phe Ala Pro Asp Lys
                280                 285                 290

cgg tta agc gcg acc cag gca ctg cag cac ccc tac gtg cag agg ttc      968
Arg Leu Ser Ala Thr Gln Ala Leu Gln His Pro Tyr Val Gln Arg Phe
            295                 300                 305

cac tgc ccc agc gac gag tgg gca cga gag gca gat gtg cgg ccc cgg     1016
His Cys Pro Ser Asp Glu Trp Ala Arg Glu Ala Asp Val Arg Pro Arg
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gca cac gaa ggg gtc cag ctc tct gtg cct gag tac cgc agc cgc gtc     1064
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Ala His Glu Gly Val Gln Leu Ser Val Pro Glu Tyr Arg Ser Arg Val
    325                 330                 335

tat cag atg atc ctg gag tgt gga ggc agc agc ggc acc tcg aga gag     1112
Tyr Gln Met Ile Leu Glu Cys Gly Gly Ser Ser Gly Thr Ser Arg Glu
340                 345                 350                 355

aag ggc ccg gag ggt gtc tcc cca agc cag gca cac ctg cac aaa ccc     1160
Lys Gly Pro Glu Gly Val Ser Pro Ser Gln Ala His Leu His Lys Pro
                360                 365                 370

aga gcc gac cct cag ctg cct tct agg aca cct gtg cag ggt ccc aga     1208
Arg Ala Asp Pro Gln Leu Pro Ser Arg Thr Pro Val Gln Gly Pro Arg
            375                 380                 385

ccc agg ccc cag agc agc cca ggc cat gac cct gcc gag cac gag tcc     1256
Pro Arg Pro Gln Ser Ser Pro Gly His Asp Pro Ala Glu His Glu Ser
        390                 395                 400

ccc cgt gca gcc aag aac gtt ccc agg cag aac tcc gct ccc ctg ctc     1304
Pro Arg Ala Ala Lys Asn Val Pro Arg Gln Asn Ser Ala Pro Leu Leu
    405                 410                 415

caa act gct ctc cta ggg aat ggg gaa agg ccc cct ggg gcg aag gaa     1352
Gln Thr Ala Leu Leu Gly Asn Gly Glu Arg Pro Pro Gly Ala Lys Glu
420                 425                 430                 435

gcg ccc ccc ttg aca ctc tcg ctg gtg aag cca agc ggg agg gga gct     1400
Ala Pro Pro Leu Thr Leu Ser Leu Val Lys Pro Ser Gly Arg Gly Ala
                440                 445                 450

gcg ccc tcc ctg acc tcc cag gct gcg gct cag gtg gcc aac cag gcc     1448
Ala Pro Ser Leu Thr Ser Gln Ala Ala Ala Gln Val Ala Asn Gln Ala
            455                 460                 465

ctg atc cgg ggt gac tgg aac cgg ggc ggt ggg gtg agg gtg gcc agc     1496
Leu Ile Arg Gly Asp Trp Asn Arg Gly Gly Gly Val Arg Val Ala Ser
        470                 475                 480

gta caa cag gtc cct ccc cgg ctt cct ccg gag gcc cgg ccc ggc cgg     1544
Val Gln Gln Val Pro Pro Arg Leu Pro Pro Glu Ala Arg Pro Gly Arg
    485                 490                 495

agg atg ttc agc acc tct gcc ttg cag ggt gcc cag ggg ggt gcc agg     1592
Arg Met Phe Ser Thr Ser Ala Leu Gln Gly Ala Gln Gly Gly Ala Arg
500                 505                 510                 515

gct ttg ctt gga ggc tac tcc caa gcc tac ggg act gtc tgc cac tcg     1640
Ala Leu Leu Gly Gly Tyr Ser Gln Ala Tyr Gly Thr Val Cys His Ser
                520                 525                 530

gca ctg ggc cac ctg ccc ctg ctg gag ggg cac cat gtg tga             1682
Ala Leu Gly His Leu Pro Leu Leu Glu Gly His His Val  *
            535                 540

gccgccctac tcccttcacc tggccctctg ttcctgcccc agccccttcc ccagacccct   1742
ctccagtctc ctgcaccccc tagccctccc tgctttgcct ggcccgttga agttccaggg   1802
agcttgcccg ggtctcctcg ggggagcaga tgagggccct gcccccgccc cactgacttt   1862
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ctccaataaa gncatgtctg ccccccccc naaaaaaaaa aaaaaaaaaa aa 1914

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<213> Homo sapiens

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35 40 45
Arg Asp Lys Thr Asp Ala Gln Arg Thr Phe Arg Glu Ile Thr Leu Leu
50 55 60
Gln Glu Phe Gly Asp His Pro Asn Ile Ile Ser Leu Leu Asp Val Ile
65 70 75 80
Arg Ala Glu Asn Asp Arg Asp Ile Tyr Leu Val Phe Glu Phe Met Asp
85 90 95
Thr Asp Leu Asn Ala Val Ile Arg Lys Gly Gly Leu Leu Gln Asp Val
100 105 110
His Val Arg Ser Ile Phe Tyr Gln Leu Leu Arg Ala Thr Arg Phe Leu
115 120 125
His Ser Gly His Val Val His Arg Asp Gln Lys Pro Ser Asn Val Leu
130 135 140
Leu Asp Ala Asn Cys Thr Val Lys Leu Cys Asp Phe Gly Leu Ala Arg
145 150 155 160
Ser Leu Gly Asp Leu Pro Glu Gly Pro Glu Asp Gln Ala Val Thr Glu
165 170 175
Tyr Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu Val Leu Leu Ser Ser
180 185 190
His Arg Tyr Thr Leu Gly Val Asp Met Trp Ser Leu Gly Cys Ile Leu
195 200 205
Gly Glu Met Leu Arg Gly Arg Pro Leu Phe Pro Gly Thr Ser Thr Xaa
210 215 220
His Gln Leu Glu Leu Ile Leu Glu Thr Ile Pro Pro Pro Ser Glu Glu
225 230 235 240
Asp Leu Leu Ala Leu Gly Ser Gly Cys Arg Ala Ser Val Leu His Gln
245 250 255
Leu Gly Ser Arg Pro Arg Gln Thr Leu Asp Ala Leu Leu Pro Pro Asp
260 265 270
Thr Ser Pro Glu Ala Leu Asp Leu Leu Arg Arg Leu Leu Val Phe Ala
275 280 285
Pro Asp Lys Arg Leu Ser Ala Thr Gln Ala Leu Gln His Pro Tyr Val
290 295 300
Gln Arg Phe His Cys Pro Ser Asp Glu Trp Ala Arg Glu Ala Asp Val
305 310 315 320
Arg Pro Arg Ala His Glu Gly Val Gln Leu Ser Val Pro Glu Tyr Arg
325 330 335
Ser Arg Val Tyr Gln Met Ile Leu Glu Cys Gly Gly Ser Ser Gly Thr
340 345 350
Ser Arg Glu Lys Gly Pro Glu Gly Val Ser Pro Ser Gln Ala His Leu

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        355                 360                 365
His Lys Pro Arg Ala Asp Pro Gln Leu Pro Ser Arg Thr Pro Val Gln
    370                 375                 380
Gly Pro Arg Pro Arg Pro Gln Ser Ser Pro Gly His Asp Pro Ala Glu
385                 390                 395                 400
His Glu Ser Pro Arg Ala Ala Lys Asn Val Pro Arg Gln Asn Ser Ala
                405                 410                 415
Pro Leu Leu Gln Thr Ala Leu Leu Gly Asn Gly Glu Arg Pro Pro Gly
            420                 425                 430
Ala Lys Glu Ala Pro Pro Leu Thr Leu Ser Leu Val Lys Pro Ser Gly
        435                 440                 445
Arg Gly Ala Ala Pro Ser Leu Thr Ser Gln Ala Ala Ala Gln Val Ala
    450                 455                 460
Asn Gln Ala Leu Ile Arg Gly Asp Trp Asn Arg Gly Gly Gly Val Arg
465                 470                 475                 480
Val Ala Ser Val Gln Gln Val Pro Pro Arg Leu Pro Pro Glu Ala Arg
                485                 490                 495
Pro Gly Arg Arg Met Phe Ser Thr Ser Ala Leu Gln Gly Ala Gln Gly
            500                 505                 510
Gly Ala Arg Ala Leu Leu Gly Gly Tyr Ser Gln Ala Tyr Gly Thr Val
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cggtggacaa agagccagcg tctgcctctc acc atg tgt gct gcc gag gtg gac      174
                                    Met Cys Ala Ala Glu Val Asp
                                     1               5

cgt cat gta tcc cag aga tac ctg atc aag cgg agg ctt ggg aag ggg      222
Arg His Val Ser Gln Arg Tyr Leu Ile Lys Arg Arg Leu Gly Lys Gly
         10                  15                  20

gcc tac ggc att gta tgg aag gcc atg gac cgg agg act ggt gag gta      270
Ala Tyr Gly Ile Val Trp Lys Ala Met Asp Arg Arg Thr Gly Glu Val
     25                  30                  35

gtg gcc atc aag aaa atc ttt gat gcc ttt agg gac cag aca gat gct      318
Val Ala Ile Lys Lys Ile Phe Asp Ala Phe Arg Asp Gln Thr Asp Ala
 40                  45                  50                  55

cag agg acc ttc cgt gaa atc atg ctt ctc cgg gag ttt ggg ggc cat      366
Gln Arg Thr Phe Arg Glu Ile Met Leu Leu Arg Glu Phe Gly Gly His
                60                  65                  70

ccc aac atc atc cgc ctg ctt gat gta atc cca gca aag aat gac agg      414
Pro Asn Ile Ile Arg Leu Leu Asp Val Ile Pro Ala Lys Asn Asp Arg
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                75                  80                  85

gat att tac ctg gtg ttt gag tcc atg gac acc gac ctg aac gcg gtc      462
Asp Ile Tyr Leu Val Phe Glu Ser Met Asp Thr Asp Leu Asn Ala Val
         90                  95                 100

atc cag aag ggc aga ctg ttg gag gac atc cac aaa cgt tgc atc ttt      510
Ile Gln Lys Gly Arg Leu Leu Glu Asp Ile His Lys Arg Cys Ile Phe
    105                 110                 115

tac cag ctc ctg aga gcc acc aag ttt atc cat tca ggg cgc gtc att      558
Tyr Gln Leu Leu Arg Ala Thr Lys Phe Ile His Ser Gly Arg Val Ile
120                 125                 130                 135

cac cgg gac cag aag cca gcc aac gtt cta ttg gat gct gct tgc cgg      606
His Arg Asp Gln Lys Pro Ala Asn Val Leu Leu Asp Ala Ala Cys Arg
                140                 145                 150

gtg aaa cta tgt gac ttt ggc ctg gca cgc tcc ctc agt gac ttc cct      654
Val Lys Leu Cys Asp Phe Gly Leu Ala Arg Ser Leu Ser Asp Phe Pro
            155                 160                 165

gaa ggc ctg ggc cag gcc ctg aca gaa tat gtg gcc aca cgc tgg tac      702
Glu Gly Leu Gly Gln Ala Leu Thr Glu Tyr Val Ala Thr Arg Trp Tyr
        170                 175                 180

cga gct cca gag gtg ctt ctg tct tcc cga tgg tat acc cct ggg gtg      750
Arg Ala Pro Glu Val Leu Leu Ser Ser Arg Trp Tyr Thr Pro Gly Val
    185                 190                 195

gac atg tgg agc ctg ggc tgc ata ctg gga gag atg ctt cga ggg cag      798
Asp Met Trp Ser Leu Gly Cys Ile Leu Gly Glu Met Leu Arg Gly Gln
200                 205                 210                 215

cca ctg ttt ccg ggt aca tct act ttc cac cag ctg gag ctg atc ctg      846
Pro Leu Phe Pro Gly Thr Ser Thr Phe His Gln Leu Glu Leu Ile Leu
                220                 225                 230

gag acc att cca ttg ccc tcc atg gag gag ctc cag ggc ctt gga tca      894
Glu Thr Ile Pro Leu Pro Ser Met Glu Glu Leu Gln Gly Leu Gly Ser
            235                 240                 245

gac tac agt gct ttg att ctg cag aat ctt gga tcc agg cca cgg cag      942
Asp Tyr Ser Ala Leu Ile Leu Gln Asn Leu Gly Ser Arg Pro Arg Gln
        250                 255                 260

acg ctg gac gcc ctc ctg ccg cca gac acc ccc cca gaa gcc ctg gac      990
Thr Leu Asp Ala Leu Leu Pro Pro Asp Thr Pro Pro Glu Ala Leu Asp
    265                 270                 275

ctc ctc aag cga ctc ttg gca ttt gct ccg gac aaa cgg ctt agt gca     1038
Leu Leu Lys Arg Leu Leu Ala Phe Ala Pro Asp Lys Arg Leu Ser Ala
280                 285                 290                 295

gag cag gct ctt caa cac cct tac gtg cag aga ttc cat tgc ccc gac     1086
Glu Gln Ala Leu Gln His Pro Tyr Val Gln Arg Phe His Cys Pro Asp
                300                 305                 310
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cgc gag tgg aca cgg ggg tcc gat gtg cgg ctc ccg gta cac gaa gga      1134
Arg Glu Trp Thr Arg Gly Ser Asp Val Arg Leu Pro Val His Glu Gly
            315                 320                 325

gac cag ctc tct gca cca gag tat cgc aac cgc ctg tac cag atg atc      1182
Asp Gln Leu Ser Ala Pro Glu Tyr Arg Asn Arg Leu Tyr Gln Met Ile
        330                 335                 340

ctg gag cgg aga cgg aac agc cgc agc cct cga gag gaa gac ttg ggg      1230
Leu Glu Arg Arg Arg Asn Ser Arg Ser Pro Arg Glu Glu Asp Leu Gly
    345                 350                 355

gtt gtg gcc tcg cgg gca gag ctc agg gct tcc cag agg caa tcg ctc      1278
Val Val Ala Ser Arg Ala Glu Leu Arg Ala Ser Gln Arg Gln Ser Leu
360                 365                 370                 375

aag ccc gga gtc ctc ccc cag gtc ttg gcg gag acg cct gcg cgg aaa      1326
Lys Pro Gly Val Leu Pro Gln Val Leu Ala Glu Thr Pro Ala Arg Lys
                380                 385                 390

cgc gga ccc aaa cct cag aat ggc cat ggt cac gat ccc gag cat gtg      1374
Arg Gly Pro Lys Pro Gln Asn Gly His Gly His Asp Pro Glu His Val
            395                 400                 405

gaa gtt cgc agg cag agt tca gac ccc ctg tac caa ctt ccg ccg cca      1422
Glu Val Arg Arg Gln Ser Ser Asp Pro Leu Tyr Gln Leu Pro Pro Pro
        410                 415                 420

ggc agc ggg gaa agg ccc cca ggg gcc aca ggg gag cca ccc tcc gca      1470
Gly Ser Gly Glu Arg Pro Pro Gly Ala Thr Gly Glu Pro Pro Ser Ala
    425                 430                 435

ccc tca ggg gtg aag act cac gtt agg gcg gtg gcg ccc tcc ctg act      1518
Pro Ser Gly Val Lys Thr His Val Arg Ala Val Ala Pro Ser Leu Thr
440                 445                 450                 455

tca cag gcc gcg gct cag gcg gcc aat cag cct ctg atc cgc agt gat      1566
Ser Gln Ala Ala Ala Gln Ala Ala Asn Gln Pro Leu Ile Arg Ser Asp
                460                 465                 470

ccg gcc cgg ggc ggt ggg cca agg gct gtc ggc gcg cga cgg gtc cct      1614
Pro Ala Arg Gly Gly Gly Pro Arg Ala Val Gly Ala Arg Arg Val Pro
            475                 480                 485

tcc cgc ctg ccc cgg gag gcc ccg gaa ccc cga ccc ggc cga agg atg      1662
Ser Arg Leu Pro Arg Glu Ala Pro Glu Pro Arg Pro Gly Arg Arg Met
        490                 495                 500

ttt ggc atc tcg gtc tcg cag ggg gcc cag ggt gca gcc aga gct gct      1710
Phe Gly Ile Ser Val Ser Gln Gly Ala Gln Gly Ala Ala Arg Ala Ala
    505                 510                 515

ctt ggc ggc tac tcc cag gcc tac ggg acc gtg tgc cgc tcc gcg ctg      1758
Leu Gly Gly Tyr Ser Gln Ala Tyr Gly Thr Val Cys Arg Ser Ala Leu
520                 525                 530                 535

ggc cgc ctg cct ctg ctc ccc gga ccg cgt gcg tga gccgcccacc           1804
Gly Arg Leu Pro Leu Leu Pro Gly Pro Arg Ala  *
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aacctccttg cggcaaactg gcgccggccc ccagacccca gcgcatcatc tcccttctct 1864
gcctccccgc cttcgagttc caggagggtt ctctgagcct ctctccccta agggggagta 1924
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aaaaaaaaaa aaaa 1998

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<213> Rattus norvegicus

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35 40 45
Phe Arg Asp Gln Thr Asp Ala Gln Arg Thr Phe Arg Glu Ile Met Leu
50 55 60
Leu Arg Glu Phe Gly Gly His Pro Asn Ile Ile Arg Leu Leu Asp Val
65 70 75 80
Ile Pro Ala Lys Asn Asp Arg Asp Ile Tyr Leu Val Phe Glu Ser Met
85 90 95
Asp Thr Asp Leu Asn Ala Val Ile Gln Lys Gly Arg Leu Leu Glu Asp
100 105 110
Ile His Lys Arg Cys Ile Phe Tyr Gln Leu Leu Arg Ala Thr Lys Phe
115 120 125
Ile His Ser Gly Arg Val Ile His Arg Asp Gln Lys Pro Ala Asn Val
130 135 140
Leu Leu Asp Ala Ala Cys Arg Val Lys Leu Cys Asp Phe Gly Leu Ala
145 150 155 160
Arg Ser Leu Ser Asp Phe Pro Glu Gly Leu Gly Gln Ala Leu Thr Glu
165 170 175
Tyr Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu Val Leu Leu Ser Ser
180 185 190
Arg Trp Tyr Thr Pro Gly Val Asp Met Trp Ser Leu Gly Cys Ile Leu
195 200 205
Gly Glu Met Leu Arg Gly Gln Pro Leu Phe Pro Gly Thr Ser Thr Phe
210 215 220
His Gln Leu Glu Leu Ile Leu Glu Thr Ile Pro Leu Pro Ser Met Glu
225 230 235 240
Glu Leu Gln Gly Leu Gly Ser Asp Tyr Ser Ala Leu Ile Leu Gln Asn
245 250 255
Leu Gly Ser Arg Pro Arg Gln Thr Leu Asp Ala Leu Leu Pro Pro Asp
260 265 270
Thr Pro Pro Glu Ala Leu Asp Leu Leu Lys Arg Leu Leu Ala Phe Ala
275 280 285
Pro Asp Lys Arg Leu Ser Ala Glu Gln Ala Leu Gln His Pro Tyr Val
290 295 300
Gln Arg Phe His Cys Pro Asp Arg Glu Trp Thr Arg Gly Ser Asp Val
305 310 315 320
Arg Leu Pro Val His Glu Gly Asp Gln Leu Ser Ala Pro Glu Tyr Arg
325 330 335
Asn Arg Leu Tyr Gln Met Ile Leu Glu Arg Arg Arg Asn Ser Arg Ser
340 345 350
Pro Arg Glu Glu Asp Leu Gly Val Val Ala Ser Arg Ala Glu Leu Arg

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Ala Ser Gln Arg Gln Ser Leu Lys Pro Gly Val Leu Pro Gln Val Leu
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Ala Glu Thr Pro Ala Arg Lys Arg Gly Pro Lys Pro Gln Asn Gly His
385                 390                 395                 400
Gly His Asp Pro Glu His Val Glu Val Arg Arg Gln Ser Ser Asp Pro
                405                 410                 415
Leu Tyr Gln Leu Pro Pro Pro Gly Ser Gly Glu Arg Pro Pro Gly Ala
            420                 425                 430
Thr Gly Glu Pro Pro Ser Ala Pro Ser Gly Val Lys Thr His Val Arg
        435                 440                 445
Ala Val Ala Pro Ser Leu Thr Ser Gln Ala Ala Ala Gln Ala Ala Asn
    450                 455                 460
Gln Pro Leu Ile Arg Ser Asp Pro Ala Arg Gly Gly Gly Pro Arg Ala
465                 470                 475                 480
Val Gly Ala Arg Arg Val Pro Ser Arg Leu Pro Arg Glu Ala Pro Glu
                485                 490                 495
Pro Arg Pro Gly Arg Arg Met Phe Gly Ile Ser Val Ser Gln Gly Ala
            500                 505                 510
Gln Gly Ala Ala Arg Ala Ala Leu Gly Gly Tyr Ser Gln Ala Tyr Gly
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Arg Ala
545
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<223> The L can also be I or V

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<223> Xaa = Any Amino Acid other than P

<221> VARIANT
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<223> Xaa = Any amino acid other than P

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<223> The F can also be Y, W, M, G, S, T, N, or H

<221> VARIANT
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<223> The S can also be G or A

<221> VARIANT
<222> (8)...(8)
<223> Xaa = Any amino acid other than P and W

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<222> (12)...(12)
<223> The G can also be S, T, A, C, L, I, V, M, F, or Y

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<223> Xaa = The next 5-18 amino acids can be any amino acid

<221> VARIANT
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<223> The L can also be I, V, M, F, Y, W, C, S, T, A, or R

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<223> The A can also be I, V, or P

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<223> The L can also be I, V, M, F, A, G, C, K, or R

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1 5 10 15
Lys

<210> 12
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<212> PRT
<213> Artificial Sequence

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<223> consensus sequence for the serine/threonine kinases

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<223> The L at position 1 can be I, V, M, F, Y, or C.

<221> VARIANT
<222> (2)...(2)
<223> The X at position 2 can be any amino acid.

<221> VARIANT
<222> (3)...(3)
<223> The H at position 3 can be Y.

<221> VARIANT
<222> (6)...(6)
<223> The L at position 6 can be I, V, M, F or Y.

<221> VARIANT
<222> (8)...(8)
<223> The X at position 8 can be any amino acid.

<221> VARIANT
<222> (9)...(9)
<223> The X at position 9 can be any amino acid.

<221> VARIANT
<222> (11)...(11)
<223> The L at position 11 can be I, V, M, F, Y, C, or
T.

<221> VARIANT
<222> (12)...(12)
<223> The L at position 12 can be I, V, M, F, Y, C, or
T.

<221> VARIANT
<222> (13)...(13)
<223> The L at position 13 can be I, V, M, F, Y, C, or
T.

<221> VARIANT
<222> (4)...(4)
<223> The X at position 4 can be any amino acid.

<400> 12
Leu Xaa His Xaa Asp Leu Lys Xaa Xaa Asn Leu Leu Leu
1 5 10

<210> 13
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence for tyrosine kinases

<221> VARIANT
<222> (1)...(1)
<223> The L at position 1 can also be I, V, M, F, Y, or

C.

<221> VARIANT
<222> (2)...(2)
<223> The X at position 2 can be any amino acid.

<221> VARIANT
<222> (3)...(3)
<223> The H at position 3 can be Y.

<221> VARIANT
<222> (6)...(6)
<223> The L at position 6 can be I, V, M, F, or Y.

<221> VARIANT
<222> (7)...(7)
<223> The R at position 7 can be S, T, A or C.

<221> VARIANT
<222> (8)...(8)
<223> The X at position 8 can be any amino acid

<221> VARIANT
<222> (9)...(9)
<223> The X at position 9 can be any amino acid

<221> VARIANT
<222> (11)...(11)
<223> The L at position 11 can be I, V, M, F, Y or C.

<221> VARIANT
<222> (12)...(12)
<223> The L at position 12 can be I, V, M, F, Y or C.

<221> VARIANT
<222> (13)...(13)
<223> The L at position 13 can be I, V, M, F, Y or C.

<221> VARIANT
<222> (4)...(4)
<223> The X at position 4 can be any amino acid.

<400> 13
Leu Xaa His Xaa Asp Leu Arg Xaa Xaa Asn Leu Leu Leu
1 5 10